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Application of Susceptible-Infected-Removed Model with Vital Dynamics for COVID-19 Outbreak in Malaysia

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HIGHLIGHTS

- A Susceptible-Infected-Recovered (SIR) model was expanded to include vital dynamics to model the outbreak of COVID-19.
- The SIR model with vital dynamics is a more realistic compared to the basic SIR model.
- The infected individuals reached their steady-state about 25 - 60 days.

ABSTRACT

In late 2019, the unique severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), also known as COVID-19, first emerged in Wuhan City, Hubei Province, China and quickly spread throughout the world. Until June 30, 2022, a total of 4,566,055 cases of COVID-19 have been reported in Malaysia, with 35,765 deaths and 4,500,856 recovered cases. This study aims to generalise a deterministic SIR model with vital dynamics for understanding the proliferation of infectious diseases. The SIR model with vital dynamics is more realistic in mimicking reality than the basic SIR model because it can determine the dynamic behaviours of COVID-19 over a more extended period. The SIR model utilises vital dynamics with unequal birth and death rates. Furthermore, the SIR model with vital dynamics is rescaled with the total time-varying population and analysed according to its epidemic condition. The results indicated that the number of infected individuals would peak about 10 - 15 days and reach their steady state about 25 - 60 days. The findings of this research may help policymakers establish, plan, and implement effective COVID-19 pandemic response strategies.

***Keywords:** COVID-19, SIR model, vital dynamics, pandemic*

INTRODUCTION

COVID-19 is not only a public health disaster but has also significantly impacted the global economy and financial markets. It was first discovered in December 2019 in Wuhan, China, causing a severe and fatal respiratory syndrome (Cooper et al., 2020). The World Health Organization (WHO) classified Coronavirus

Disease 2019 (COVID-19) as a pandemic on March 11, 2020, due to the disease's rapid and widespread transmission (dos Santos, 2020). On January 25, 2020, Malaysia reported its first case of COVID-19, which was brought by three Chinese nationals who had just been to Singapore and had close contact with an infected individual (Elengoe, 2020). Since then, there has been a significant increase in the total number of cases. As of June 30, 2022, there are 4,566,055 positive COVID-19 cases, with 35,765 fatalities and 4,500,856 recovered cases.

Mathematical models have been developed and applied in mathematical epidemiology to explore the transmission of infectious illnesses since the early 20th century (Trawicki, 2017). Compartmental models are epidemiological studies that divide a population into groups, and the SIR model is the most often utilised of these models. In 1927, Kermack and McKendrick (1927) introduced the SIR model, one of the most straightforward yet powerful disease models for modelling infectious diseases in mathematical epidemiology. Later studies have adjusted the SIR model to accommodate the current state of infectious diseases.

Much research on COVID-19 has utilised this model to understand how the disease spreads, anticipate pandemic peaks, and evaluate quarantine measures. Muñoz-Fernández et al. (2021) showed that a basic SIR-type model with non-constant parameters could model the COVID-19 course in Italy, Spain, and the United States. They also demonstrated that by selecting a suitable transmission function, they could make multiple forecasts and receive highly realistic results. Cooper et al. (2020) developed a SIR model with vital dynamics to investigate the spread of COVID-19 in the community. The suggested model successfully models and forecasts the virus's transmission in communities. In Malaysia, Ariffin et al. (2021) assessed the predictive capability of the SIR model on the trajectory of COVID-19. Their findings demonstrated that the simulated trend could effectively replicate the actual count and retain the actual spikes. It is motivated by the lack of studies on using the SIR model with vital dynamics in Malaysia and the fact that the SIR model with vital dynamics is more realistic in mimicking reality than the basic SIR model, we proposed a deterministic SIR model with vital dynamics for understanding the proliferation of infectious diseases in Malaysia. This study's remaining section is structured as follows: we introduce the SIR model with vital dynamics in Section 2. Then, in Section 3, we present the result of our analysis for Malaysia. Finally, in Section 4, we wrap up our work and review the findings of our study.

METHODOLOGY

This study modifies a classic SIR model by introducing births and deaths due to natural causes into the model. The SIR model with vital dynamics is considered with an initial total population size of *N*. The transitions between disease states are described as follows:

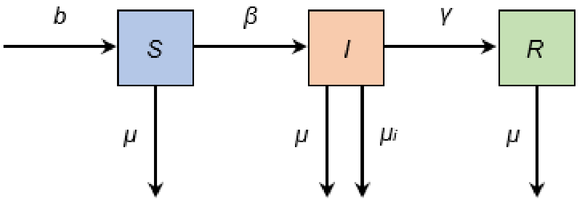

Figure 1: The SIR model with vital dynamics

The mathematical formula that describes the disease dynamics is given by the following system of ordinary differential equations (ODEs), where the initial conditions are nonnegative:

$$\frac{dS}{dt} = bN - \mu S - \beta SI$$
$$\frac{dI}{dt} = \beta SI - \mu I - \mu_i I - \gamma I \qquad (1)$$
$$\frac{dR}{dt} = \gamma I - \mu R$$

where S, I, and R represent the susceptible population, infected population and recovered population respectively. The term b refers as the birth rate, μ is the natural mortality rate, μ_i is the death rate caused by the disease, β is the contact rate, and γ is the recovery rate. Therefore, $S(0) = N(0) - I(0) - R(0)$, $I(0) \geq 1$, $R(0) \geq 0$, and population over time is $N(t) = S(t) + I(t) + R(t)$.

Trawicki (2017) states that the SIR model can accommodate vital dynamics with unequal birth and death rates. With today's population, it is assumed that all newborns and people are susceptible. The susceptible population is then infected due to the interaction of susceptible and infected individuals. Without an effective vaccine to cure infected individuals, they will recover from the infectious disease and join the recovered population.

Assumptions of the SIR Model with Vital Dynamics

This model is appropriate under the following assumptions:

i) All new-borns fall into the susceptible category.
ii) The natural birth and death rates are included.
iii) The only option to leave the susceptible group is to get infected or die naturally.
iv) Immunity is granted after an individual has recovered.
v) The recovered individual cannot spread disease to others.

FINDINGS AND DISCUSSIONS

The proposed SIR model with vital dynamics was evaluated in Python. Table 1 below lists a set of numerical values of the parameter.

Table 1: Parameter Values

Parameter	Description	Value	Source
$N(0)$	Initial total population	32.45×10^6	(Department of Statistics Malaysia, 2020)
$S(0)$	Initial susceptible population	32.33×10^6	(Worldometer, 2020)
$I(0)$	Initial infected population	115,078	(Worldometer, 2020)
$R(0)$	Initial recovered population	91,171	(Worldometer, 2020)

$\boldsymbol{b}$	Birth rate	3.95×10^{-5}	(Department of Statistics Malaysia, 2020)
$\boldsymbol{\mu}$	Natural mortality rate	1.40×10^{-5}	(Department of Statistics Malaysia, 2020)
$\boldsymbol{\mu_i}$	Death rate caused by the disease	0.0039	(Worldometer, 2020)
$\boldsymbol{\beta}$	Infection rate	0.11	(Salman et al., 2021)
$\boldsymbol{\gamma}$	Recovery rate	0.07	(Lechien et al., 2020)

Simulations were performed using the proposed and rescaled SIR model with vital dynamics in Equation 1 along with the parameter values in Table 1. Figure 2 shows the SIR model for the rescaled variables against time in days for 180 days.

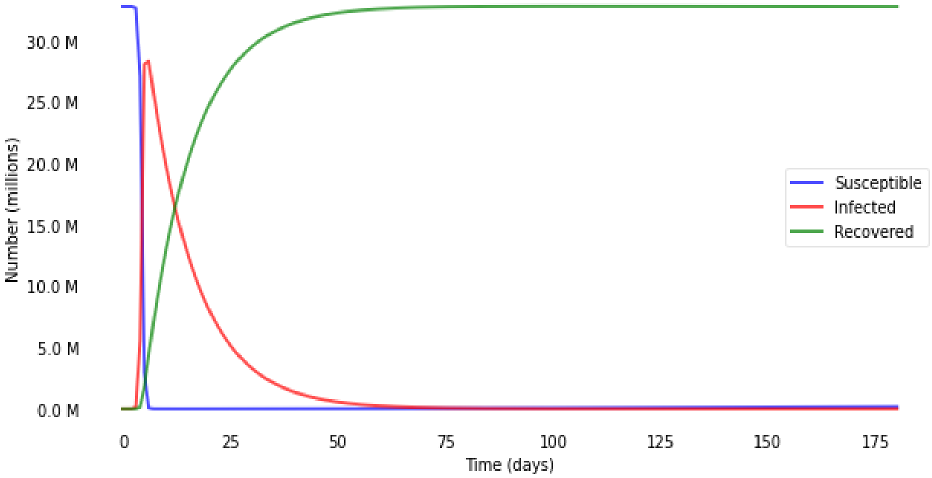

Figure 2: Simulation of the proposed SIR model with vital dynamics

The simulation shows that the number of infected individuals would peak about 10 – 15 days and reach their steady state about 25 – 60 days. The susceptible individuals have reached a steady state on approximately ten days, while the recovered individuals have approximately 40 days. Our simulation indicates that a pandemic is unavoidable, and this finding aligns with that period's situation.

The effective contact rate, β, and the recovery rate, γ, are two critical criteria for preventing disease transmission. As a result, it determines the number of persons in a given population compartment. These two usually function in tandem to counteract or nullify each other. For example, if one decreases, the other grows, and vice versa. Increasing the effective contact rate (which indicates disease transmission) while reducing the recovery rate increased the number of infected compartments in the population over time. On the other hand, while the effective contact rate is lowered, an increase in the recovery rate (signifying illness reduction) increases the number of the susceptible population over time.

However, the effective contact rate might be frequency or mass action dependent, while the recovery rate is determined by vaccination and isolation. For example, suppose transmission of COVID-19 depends on the number of times the infected individuals come into touch with susceptible persons in the community;

the effective contact rate is said to depend on the frequency of transmission. Therefore, these two factors are always considered when it comes to eliminating epidemics.

CONCLUSION AND RECOMMENDATIONS

This model is designed and developed for understanding the proliferation of COVID-19 in Malaysia. The simulation shown that the pandemic is unpreventable. In order to stop the pandemic from spreading further, the authorities will need to implement several treatments and preventative steps. Furthermore, non-pharmaceutical intervention measures such as wearing masks in confined spaces or where crowds are anticipated, as well as isolation, should remain mandatory. These intervention approaches will slow the rate of COVID-19 transmission in communities, keeping healthcare services at capacity. Finally, our mathematical modelling technique may assist policymakers in creating, planning, and implementing key pandemic-fighting efforts.

Additional factors should be considered in future research when modelling COVID-19 transmission. For example, it can consider the infected person's lifestyle, which is thought to have influenced the transmission rate via social contacts. In addition, future studies can also consider the population changing (rather than remaining stable) due to migration and other factors contributing to population changes. The SIR model used in this study only included the human-to-human transmission rate. Future studies should include additional factors affecting disease spread to improve the findings. As a result, the study recommends that more research be done into the model's other parameters.

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CONFLICT OF INTEREST DISCLOSURE

All authors declare that they have no conflicts of interest to disclose.

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